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(54) **GENE SIGNATURE.**

(57) A 3'-directed cDNA library which accurately reflects the abundance ration of mRNA in a cell has been prepared from various human tissues, and sequencing of the cDNAs contained in the library has be conducted to examine the incidence of each cDNA in each tissue. As each cDNA has expression information with each tissue corresponding to the mRNA concentration, these cDNAs are usable as a probe or primer for detecting cell anomaly or discriminating cells. The cloned gene can produce portoins utilizable as a medicine or the like.

EP 0 679 716 A1

EP 0 679 716 A1

CLONE:HUMGS08334

SEQUENCE DESCRIPTION:

5 GATCAGACTT TTGNTCTTG GGTCCCAGAT GGCACAGGAG CACTGCATGC TTGTTTTCTA 60
 GAGCCCAGCC AGTCATGGGT GCTAGCCTAG TCTCCACACA CCAGCAAGTA GAACCCAAGT 120
 GTANNNNNAT AAATATTTCC TGAGTACCAG TAAGAGAATG CATTCTTTTC TCATCTAGGC 180
 CAGGAATGTT GAAAATGCTC AGCCTTACAT AGAAACTCCT AGATTTTCAC TAACGCATTT 240
 CACAAAAGTA AATAAGTATT TCATATAATT CAGAGGATGT TTAAATTGTC AGCATTTTAA 300
 TAAATAN 307

SEQ ID NO:7099

SEQUENCE LENGTH:199

SEQUENCE TYPE:nucleic acid

15 TOPOLOGY:linear

CLONE:HUMGS08335

SEQUENCE DESCRIPTION:

20 GATCTGTACT TTGAACAAAG AAAAGTGTGA GAGACCCCTG GGAGTGAGGG GTAGGGGATA 60
 CAATACTCTG AAGCAGAAGA GGACCTTGC AGTGATGGTT AGGGACTCTT CTGAGTAGGA 120
 GACGTAATCG GCTTTTGGTC CATGGAACCT TTACCACATG TATTCAGCAT ATATACACGA 180
 TTAAAGTGCT GCAAAATAA 199

SEQ ID NO:7100

SEQUENCE LENGTH:297

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08336

SEQUENCE DESCRIPTION:

30 GATCTGGGAG TGGCTTCCTA ACGGAAATGG AACAGGATTA CCAACTAGTN GACGAAAGTA 60
 ATGCTTTCCA TGACAACCTT AGGTCTCTTG ACAGNAATCT GCCCTCAGAC AGCCAGGACT 120
 TGGGTCAACA TGGATTAGAA GAGGATTTNA TGTTATAAAA GAGGATTTTC CCACCTTGAC 180
 ACCAGGCAAT GTAGTTAGCA TATTTANNGT ACCATGGTTA TATGATTAAT CTTGGGACAA 240
 AGAATTTNAT AGAAATTTTT AAACATCTGA AAAAGAAGCT TAAGTTTAT CATCCTN 297

SEQ ID NO:7101

SEQUENCE LENGTH:296

SEQUENCE TYPE:nucleic acid

40 TOPOLOGY:linear

CLONE:HUMGS08337

SEQUENCE DESCRIPTION:

45 GATCTTTGTC TGTGAAGAAG AAAATTATCT CCCTAGTTCA ATCTGTAGTG AAATAAGGCT 60
 ACAGAAGGCA TTGTTTTTTC CTTTTNATT TTTTGATTA TATATTTNCC TTAAATATGT 120
 TTTATTGTCT TCTCTANGCA AAAAGTTCTT AATAANCATA GTATTTCTCT CTGCGTCTTA 180
 TTTCAATAGT GAAGACATAG TTCACCTAAA ATGGCATCCT GCTCTGAATC TAGNCTTTTT 240
 AGAAATGGCA TATGGTTTTG ATGATATGNC CACCATCCAA AATGTCCGAN TNAATN 296

50 SEQ ID NO:7102

EP 0 679 716 A1

SEQUENCE LENGTH:305

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08338

SEQUENCE DESCRIPTION:

GATCAACTTT AAGAAGATT ACAAAACGCT CAAGAAAGAN GAGGATATCC NACTNTTCCC 60
CGTGCAGACA AAATACATGG ATGTGGTCAA NGAGTGAATC CGTTTAGCTC GACAGATTGA 120
GAAATCTGAG TATCGGAAC TCCAGGCTTG CCTNCACAAC TCTTGGATTG AGCAGGCAGC 180
AGCTGCCCTG GAGATTGAGC TGGAAGANGA CATGTATAAG GNAGGAAAAG CTNNCCAGCA 240
AGAAGAACGT CGGNGACAAA AGCAGATGGN GGTTCNGAA GAAGGAGCTG CGNCNCCTGC 300
TTNTN 305

SEQ ID NO:7103

SEQUENCE LENGTH:414

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08339

SEQUENCE DESCRIPTION:

GATCCACAAG TCCTTGTCC ACTGTGCCTT GGTTCCTCCT TTATTTCTAA GTGGAAAAAG 60
TATTAGCCAC CATCTNACCT CACAGTGATG TTGTGAGGAC ATGTGGAAGC ACTTTAAGTT 120
TTTTCATCAT AACATAAATN ATTTTCAAGT GTAACCTATT AACCTATTTA TTATTTATGT 180
ATTTATTTAA GCATCAAATA TTTGTGCAAG AATTGGAAG AATAGANGAT GAATCATTGA 240
TTGANTAGTT ATAAAGATGT TATAGTAAAT TNATTTTATT TTAGATATTA AATGATGTTT 300
TATTAGGATA AATTCAATC AGGGTTTTTN GGATTAANCA ACCANCCAAT TGGGTCCCCA 360
GTTAANTTTC CATTCAGAT ANCCACCANN TAGTTTCNNN GTNTAGGTCC ATTN 414

SEQ ID NO:7104

SEQUENCE LENGTH:252

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08340

SEQUENCE DESCRIPTION:

GATCCCCTGA CTGGCTGGGG GCAGCTCCCA GGATATCCTG CCTTCCAACT GTTCTGAAG 60
CGCCTCCTCC TAACATGGCG ATTCCGGAGG TCAAGNCCNT GGGCTCTCCC CAGGGTCTAA 120
CGGTAAAGGT GACCACATAC CAGTGCCAAG GGGNTTNTAA AGTGGTGATG TAGTTNTGCT 180
CCCCTCCCCA AGAGCGGGTG GNGGGGGGTT NAANATGTTT GGCCTGNNTA AGTGGGCCTT 240
CCCATTNAAG TN 252

SEQ ID NO:7105

SEQUENCE LENGTH:318

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS08341

SEQUENCE DESCRIPTION:

GATCTTATTT TTTAATTTTA AGTGCCACTA TTAATGTAAA AAGGGGGGGG CTCTACAGCA 60

EP 0 679 716 A1

5 GTCGTGATGA AACTTAAATA TATATCCTTT GTCCTCGAGA TTTTAGGAAG GGTGTAGGGT 120
 GAGTAGGCCA TTTTNAATTN CTGAAGTGCT AAGTGTTTTT ATACAGCAAA CAAAAAGTCA 180
 ATTTTCCTTT CCACCAGTGC GAGAGAGGAT GTATACTTN CAAGAGAGAT GATTGCCTAT 240
 TTNCCGTTT ACAGAGTCCC GTAGATGAGC AATGGGGAAC TGGTTGCCAG GGTCTAANTT 300
 TGGATTGATT TATGCACN 318

10 SEQ ID NO:7106
 SEQUENCE LENGTH:299
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08342
 SEQUENCE DESCRIPTION:
 15 GATCTGTGAC CCCAGCCATG AGGACCCTCG CCATCCTTGC TGCCATTCTC CTGGTGGCCC 60
 TGCAGGCCCA GGCTGAGCCA CTCCAGGCAA GAGCTGATGA GGTGCTGCA GCCCCGGAGC 120
 AGATTGCAGC GGACATCCCA GAAGTGGTTG TTTCCCTTGC ATGGGACGAA AGCTTGGCTC 180
 CAAAGCATCC AGGCTCAAGG AAAACATGG CCTGCTATTG CAGAATACCA GCGTGCATTG 240
 20 CAGGAGAACG TCGCTATGGA ACCTGCATCT ACCAGGGAAG ACTCTGGGCA TTCTGCTTN 299

25 SEQ ID NO:7107
 SEQUENCE LENGTH:302
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 CLONE:HUMGS08343
 SEQUENCE DESCRIPTION:
 30 GATCTTAGAG GTTGAAGCCC ACCTTCTCTT TTCACATAGG AGGGAACAGA CCATGGAAAT 60
 TTAACGACT TCCTCAGGT CACAGAACTA GTTTTTAAT CCTCAGGCAG TGNATCCCC 120
 CACCTACAA CTGTGCACAA CCTCTTCCC CACAGTGCAA TTCAGAATAT GCTCAGGGAA 180
 TGCCAGGCAC CTTGTAAAAC TGCTGGGAGA AAAGCATGNT TCCCACAAGG ACTAAGTATC 240
 AGTGATTGT AATTTTCTG TTTGTATTA TCTGCTTGC TGATGTAGAC AAGAGTTAAC 300
 TN 302

35 SEQ ID NO:7108
 SEQUENCE LENGTH:110
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 40 CLONE:HUMGS08344
 SEQUENCE DESCRIPTION:
 GATCNAACTG TCTCACTGCT TTTCCAACTA TAATCATNTC GCTCTNACTT TAACAAAAGG 60
 CGATGGCACA GTAATTTAGT AAATTTNTGT AATAACATNT AAAAAAAGN 110

45 SEQ ID NO:7109
 SEQUENCE LENGTH:121
 SEQUENCE TYPE:nucleic acid
 TOPOLOGY:linear
 50 CLONE:HUMGS08345

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